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#10



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RAW SEQUENCE LISTING

DATE: 02/28/2002

PATENT APPLICATION: US/09/963,790A

TIME: 11:21:53

Input Set : A:\032301.230.SEQ.ST25.txt

Output Set: N:\CRF3\02282002\I963790A.raw

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3 <110> APPLICANT: FARWICK, Mike, et al.
5 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE dead GENE
7 <130> FILE REFERENCE: 032301 WD 230
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/963,790A
C--> 9 <141> CURRENT FILING DATE: 2001-09-27
9 <160> NUMBER OF SEQ ID NOS: 4
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 2381
15 <212> TYPE: DNA
16 <213> ORGANISM: Corynebacterium glutamicum
18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (259)..(2130)
21 <223> OTHER INFORMATION:
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25 caggaaaccc cgcagggtga ctcagcatca gctgacttcg ctctcgaaac cccaaccaac      60
27 actgttgaag atgcaccagc atctgagggt agcgaagaga tcaccagggt tgcggatact      120
29 tctgaggacg cgcactctgc agatgcagac aacgcgagca atgtaatcaa tgagaatgag      180
31 gactcctcgg aaggtgctaa ccagccttca aacgagtcac cctctacgga agccaaatcc      240
33 ggcttcgatg cactcgga ctg oca gag cgt gta ctt gac gct gtg cgc aag      291
34                               Met Pro Glu Arg Val Leu Asp Ala Val Arg Lys
35                               1           5           10
37 gtg ggt tac gaa act cct tcc cca att cag gca caa acc atc cca atc      339
38 Val Gly Tyr Glu Thr Pro Ser Pro Ile Gln Ala Gln Thr Ile Pro Ile
39                               15           20           25
41 ctc atg gag ggc cag gat gtt gtt ggt cta gca cag acc ggt acc ggt      387
42 Leu Met Glu Gly Gln Asp Val Val Gly Leu Ala Gln Thr Gly Thr Gly
43                               30           35           40
45 aag act gca gct ttc gcg ctg cca atc ctt gcc cgt att gac aag tcc      435
46 Lys Thr Ala Ala Phe Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser
47                               45           50           55
49 gtg cgc agc cca cag gca ctt gtg ctt gcc cct acc cgt gag cag gca      483
50 Val Arg Ser Pro Gln Ala Leu Val Leu Ala Pro Thr Arg Glu Gln Ala
51 60           65           70           75
53 ctt cag gtt gct gac tcc ttc caa tcc ttc gct gac cac gtc ggt ggc      531
54 Leu Gln Val Ala Asp Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly
55                               80           85           90
57 ctg aac gtt ctg cca atc tat ggt gga cag gct tac ggc att cag ctc      579
58 Leu Asn Val Leu Pro Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu
59                               95           100          105
61 tct ggc ctg cgt cgt ggc gct cac atc gtc gtg ggt acc cca ggc cga      627
62 Ser Gly Leu Arg Arg Gly Ala His Ile Val Val Gly Thr Pro Gly Arg

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63	110	115	120	
65	atc atc gat cac ctc gaa aag ggc tcc ctg gat atc tcc gga ctg cgc	675		
66	Ile Ile Asp His Leu Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg			
67	125 130 135			
69	ttc ctc gtg ctc gat gaa gca gac gag atg ctg aac atg ggc ttc cag	723		
70	Phe Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Met Gly Phe Gln			
71	140 145 150 155			
73	gaa gat gtc gag cgc atc ctc gag gac acc cca gac gag aag cag gtt	771		
74	Glu Asp Val Glu Arg Ile Leu Glu Asp Thr Pro Asp Glu Lys Gln Val			
75	160 165 170			
77	gca cta ttc tcc gca acg atg cca aac ggc att cgt cgc ctg tcc aag	819		
78	Ala Leu Phe Ser Ala Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys			
79	175 180 185			
81	cag tac ctg aac aac cct gct gaa atc acc gtt aag tcc gag acc agg	867		
82	Gln Tyr Leu Asn Asn Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg			
83	190 195 200			
85	act aac acc aac atc acc cag cgc ttc ctc aac gtt gca cac cgc aac	915		
86	Thr Asn Thr Asn Ile Thr Gln Arg Phe Leu Asn Val Ala His Arg Asn			
87	205 210 215			
89	aag atg gat gca ctg acc cgt att ctc gag gtc acc gag ttt gaa gca	963		
90	Lys Met Asp Ala Leu Thr Arg Ile Leu Glu Val Thr Glu Phe Glu Ala			
91	220 225 230 235			
93	atg atc atg ttc gtg cgc acc aag cac gaa act gaa gaa gtt gct gaa	1011		
94	Met Ile Met Phe Val Arg Thr Lys His Glu Thr Glu Glu Val Ala Glu			
95	240 245 250			
97	aag ctc cgt gca cgc gga ttc tcc gca gca gcc atc aac ggc gac att	1059		
98	Lys Leu Arg Ala Arg Gly Phe Ser Ala Ala Ala Ile Asn Gly Asp Ile			
99	255 260 265			
101	gct cag gca cag cgt gag cgc acc gtc gac cag ctg aag gac ggc cgc	1107		
102	Ala Gln Ala Gln Arg Glu Arg Thr Val Asp Gln Leu Lys Asp Gly Arg			
103	270 275 280			
105	ctg gac atc ctc gtt gca acc gac gtt gca gcc cgt ggt ctt gac gtt	1155		
106	Leu Asp Ile Leu Val Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Val			
107	285 290 295			
109	gag cgc atc tcc cac gtg ctt aac ttc gac att cca aac gac acc gag	1203		
110	Glu Arg Ile Ser His Val Leu Asn Phe Asp Ile Pro Asn Asp Thr Glu			
111	300 305 310 315			
113	tcc tac gtt cac cgc atc ggc cgc acc ggc cgt gca gga cgt acc ggc	1251		
114	Ser Tyr Val His Arg Ile Gly Arg Thr Gly Arg Ala Gly Arg Thr Gly			
115	320 325 330			
117	gag gca atc ctg ttc gtg acc cca cgt gag cgt cgt atg ctt cgc tcc	1299		
118	Glu Ala Ile Leu Phe Val Thr Pro Arg Glu Arg Arg Met Leu Arg Ser			
119	335 340 345			
121	atc gag cgc gca acc aac gca cca ctg cac gaa atg gaa ctg cca acc	1347		
122	Ile Glu Arg Ala Thr Asn Ala Pro Leu His Glu Met Glu Leu Pro Thr			
123	350 355 360			
125	gtc gat cag gtc aac gac ttc cgc aag gtc aag ttc gct gac tcc atc	1395		
126	Val Asp Gln Val Asn Asp Phe Arg Lys Val Lys Phe Ala Asp Ser Ile			
127	365 370 375			

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129 acc aag tcc ctc gag gac aag cag atg gac ctg ttc cgc acc ctg gtc      1443
130 Thr Lys Ser Leu Glu Asp Lys Gln Met Asp Leu Phe Arg Thr Leu Val
131 380                      385                      390                      395
133 aag gaa tac tcc cag gcc aac gac gtt cct cta gag gac atc gca gcg      1491
134 Lys Glu Tyr Ser Gln Ala Asn Asp Val Pro Leu Glu Asp Ile Ala Ala
135                      400                      405                      410
137 gca ctg gca acc cag gca cag tcc ggc gac ttc ctg ctc aag gag ctc      1539
138 Ala Leu Ala Thr Gln Ala Gln Ser Gly Asp Phe Leu Leu Lys Glu Leu
139                      415                      420                      425
141 cca cca gag cgc cgt gag cgc aac gac cgc cgt cgt gac cgt gac ttc      1587
142 Pro Pro Glu Arg Arg Glu Arg Asn Asp Arg Arg Arg Asp Arg Asp Phe
143                      430                      435                      440
145 gac gac cgt ggt gga cgt gga cgc gac cgt gac cgt ggc gac cgc gga      1635
146 Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Arg Gly Asp Arg Gly
147                      445                      450                      455
149 gat cgt ggc tca cgc ttc gac cgc gac gac gag aac ctg gca acc tac      1683
150 Asp Arg Gly Ser Arg Phe Asp Arg Asp Asp Glu Asn Leu Ala Thr Tyr
151 460                      465                      470                      475
153 cgc ctc gca gtg ggc aag cgc cag cac atc cgc cca ggc gca atc gtt      1731
154 Arg Leu Ala Val Gly Lys Arg Gln His Ile Arg Pro Gly Ala Ile Val
155                      480                      485                      490
157 ggt gca ctt gcc aac gaa ggt ggc ctg aac tcc aag gac ttc ggc cgc      1779
158 Gly Ala Leu Ala Asn Glu Gly Gly Leu Asn Ser Lys Asp Phe Gly Arg
159                      495                      500                      505
161 atc acc atc gca gcc gac cac acc ctg gtt gaa ctg cca aag gat ctc      1827
162 Ile Thr Ile Ala Ala Asp His Thr Leu Val Glu Leu Pro Lys Asp Leu
163                      510                      515                      520
165 cca cag agc gtt ctt gac aac ctg cgc gac acc cgc atc tcc ggc cag      1875
166 Pro Gln Ser Val Leu Asp Asn Leu Arg Asp Thr Arg Ile Ser Gly Gln
167                      525                      530                      535
169 ctc atc aac ata gaa cgc gac tcc ggt gga cgc cca cca cgc cgc ttc      1923
170 Leu Ile Asn Ile Glu Arg Asp Ser Gly Gly Arg Pro Pro Arg Arg Phe
171 540                      545                      550                      555
173 gag cgc gat gac cgt ggc gga cgc ggc gga ttc cgc ggc gac cgt gat      1971
174 Glu Arg Asp Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Asp Arg Asp
175                      560                      565                      570
177 gac cgc ggt gga cgt gga cgt gac cgt gac gat cgt gga agc cgt gga      2019
178 Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Asp Arg Gly Ser Arg Gly
179                      575                      580                      585
181 ggt ttc cgc ggt gga cgt gac cgt gat cgt ggc gga cgc ggt gga      2067
182 Gly Phe Arg Gly Gly Arg Asp Arg Asp Asp Arg Gly Gly Arg Gly Gly
183                      590                      595                      600
185 ttc cgc gga cgc gac gac cgc gga gac cgt ggt ggc cgt ggc ggt tac      2115
186 Phe Arg Gly Arg Asp Asp Arg Gly Asp Arg Gly Gly Arg Gly Gly Tyr
187                      605                      610                      615
189 cgt ggc gga cgc gac taagagttcg ttttagcttc agctcagggtt ttgcctgag      2170
190 Arg Gly Gly Arg Asp
191 620
193 tctggtgctt agctagaaaa atccgttgct ctctctttac tgagagggca acggattttt      2230

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195 tctgttttct taggcttttg ttcttggggg atcttggggg aggaattcta ggaacttaga 2290
197 gaagtaaattg atggtgcttc gaccgcagca ccatcgtaa gattctgacc aaagaagaga 2350
199 gcattgcgtt gctctctagt cagagtgcga g 2381
202 <210> SEQ ID NO: 2
203 <211> LENGTH: 624
204 <212> TYPE: PRT
205 <213> ORGANISM: Corynebacterium glutamicum
207 <400> SEQUENCE: 2
209 Met Pro Glu Arg Val Leu Asp Ala Val Arg Lys Val Gly Tyr Glu Thr
210 1 5 10 15
213 Pro Ser Pro Ile Gln Ala Gln Thr Ile Pro Ile Leu Met Glu Gly Gln
214 20 25 30
217 Asp Val Val Gly Leu Ala Gln Thr Gly Thr Gly Lys Thr Ala Ala Phe
218 35 40 45
221 Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser Val Arg Ser Pro Gln
222 50 55 60
225 Ala Leu Val Leu Ala Pro Thr Arg Glu Gln Ala Leu Gln Val Ala Asp
226 65 70 75 80
229 Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly Leu Asn Val Leu Pro
230 85 90 95
233 Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu Ser Gly Leu Arg Arg
234 100 105 110
237 Gly Ala His Ile Val Val Gly Thr Pro Gly Arg Ile Ile Asp His Leu
238 115 120 125
241 Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg Phe Leu Val Leu Asp
242 130 135 140
245 Glu Ala Asp Glu Met Leu Asn Met Gly Phe Gln Glu Asp Val Glu Arg
246 145 150 155 160
249 Ile Leu Glu Asp Thr Pro Asp Glu Lys Gln Val Ala Leu Phe Ser Ala
250 165 170 175
253 Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys Gln Tyr Leu Asn Asn
254 180 185 190
257 Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg Thr Asn Thr Asn Ile
258 195 200 205
261 Thr Gln Arg Phe Leu Asn Val Ala His Arg Asn Lys Met Asp Ala Leu
262 210 215 220
265 Thr Arg Ile Leu Glu Val Thr Glu Phe Glu Ala Met Ile Met Phe Val
266 225 230 235 240
269 Arg Thr Lys His Glu Thr Glu Glu Val Ala Glu Lys Leu Arg Ala Arg
270 245 250 255
273 Gly Phe Ser Ala Ala Ala Ile Asn Gly Asp Ile Ala Gln Ala Gln Arg
274 260 265 270
277 Glu Arg Thr Val Asp Gln Leu Lys Asp Gly Arg Leu Asp Ile Leu Val
278 275 280 285
281 Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Val Glu Arg Ile Ser His
282 290 295 300
285 Val Leu Asn Phe Asp Ile Pro Asn Asp Thr Glu Ser Tyr Val His Arg
286 305 310 315 320
289 Ile Gly Arg Thr Gly Arg Ala Gly Arg Thr Gly Glu Ala Ile Leu Phe

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290          325          330          335
293 Val Thr Pro Arg Glu Arg Arg Met Leu Arg Ser Ile Glu Arg Ala Thr
294          340          345          350
297 Asn Ala Pro Leu His Glu Met Glu Leu Pro Thr Val Asp Gln Val Asn
298          355          360          365
301 Asp Phe Arg Lys Val Lys Phe Ala Asp Ser Ile Thr Lys Ser Leu Glu
302          370          375          380
305 Asp Lys Gln Met Asp Leu Phe Arg Thr Leu Val Lys Glu Tyr Ser Gln
306 385          390          395          400
309 Ala Asn Asp Val Pro Leu Glu Asp Ile Ala Ala Ala Leu Ala Thr Gln
310          405          410          415
313 Ala Gln Ser Gly Asp Phe Leu Leu Lys Glu Leu Pro Pro Glu Arg Arg
314          420          425          430
317 Glu Arg Asn Asp Arg Arg Arg Asp Arg Asp Phe Asp Asp Arg Gly Gly
318          435          440          445
321 Arg Gly Arg Asp Arg Asp Arg Gly Asp Arg Gly Asp Arg Gly Ser Arg
322          450          455          460
325 Phe Asp Arg Asp Asp Glu Asn Leu Ala Thr Tyr Arg Leu Ala Val Gly
326 465          470          475          480
329 Lys Arg Gln His Ile Arg Pro Gly Ala Ile Val Gly Ala Leu Ala Asn
330          485          490          495
333 Glu Gly Gly Leu Asn Ser Lys Asp Phe Gly Arg Ile Thr Ile Ala Ala
334          500          505          510
337 Asp His Thr Leu Val Glu Leu Pro Lys Asp Leu Pro Gln Ser Val Leu
338          515          520          525
341 Asp Asn Leu Arg Asp Thr Arg Ile Ser Gly Gln Leu Ile Asn Ile Glu
342          530          535          540
345 Arg Asp Ser Gly Gly Arg Pro Pro Arg Arg Phe Glu Arg Asp Asp Arg
346 545          550          555          560
349 Gly Gly Arg Gly Gly Phe Arg Gly Asp Arg Asp Asp Arg Gly Gly Arg
350          565          570          575
353 Gly Arg Asp Arg Asp Asp Arg Gly Ser Arg Gly Gly Phe Arg Gly Gly
354          580          585          590
357 Arg Asp Arg Asp Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Arg Asp
358          595          600          605
361 Asp Arg Gly Asp Arg Gly Gly Arg Gly Gly Tyr Arg Gly Gly Arg Asp
362          610          615          620

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365 <210> SEQ ID NO: 3

366 <211> LENGTH: 28

367 <212> TYPE: DNA

368 <213> ORGANISM: Corynebacterium glutamicum

370 <400> SEQUENCE: 3

371 gatctagaaa tccggcttcg atgcactc

28

374 <210> SEQ ID NO: 4

375 <211> LENGTH: 28

376 <212> TYPE: DNA

377 <213> ORGANISM: Corynebacterium glutamicum

379 <400> SEQUENCE: 4

380 ctaagcttcg acggttgga gttccatt

28

VERIFICATION SUMMARY

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Input Set : A:\032301.230.SEQ.ST25.txt

Output Set: N:\CRF3\02282002\I963790A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date